

AMENDMENTS TO THE DRAWINGS:

Replacement drawing sheets showing amended Figures 1, 3, 9D, 10A and 10D, without markings, is attached herewith on a separate sheet in compliance with §1.84(p)(5).

Annotated drawing sheets showing amended Figures 1, 3, 9D, 10A and 10D, with markings, is attached herewith on a separate sheet in compliance with §1.84(p)(5).

REMARKS

Entry of the foregoing, and early and favorable consideration of the subject application on the merits are respectfully requested.

By the present Amendment, the specification has been amended to incorporate a revised sequence listing, and to insert SEQ ID numbers into the specification and claims. Claim 37 is amended to clarify that the DNA encodes a polypeptide. No new matter has been added.

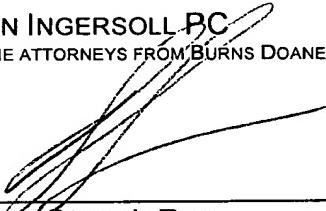
In the event that there are any questions concerning this Amendment, or the application in general, the Examiner is respectfully urged to telephone Applicants' undersigned representative, so that prosecution of the application may be expedited.

Respectfully submitted,

BUCHANAN INGERSOLL PC
(INCLUDING THE ATTORNEYS FROM BURNS DOANE SWECKER & MATHIS)

Date: December 7, 2005

By:


Teresa Stanek Rea
Registration No. 30,427

P.O. Box 1404
Alexandria, Virginia 22313-1404
(703) 836-6620

Enclosures: Five (5) sheets of Replacement drawings (FIGS. 1, 3, 9D, 10A and 10D)

Five (5) sheets of Annotated drawings showing changes (FIGS. 1, 3, 9D, 10A and 10D)

ANNOTATED SHEET SHOWING CHANGES

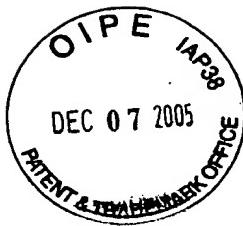
Application No. 09/900,963

Attorney Docket No.: 010830-118

Inventor(s): Claudine Guerin-Marchand et al.

PEPTIDE SEQUENCES SPECIFIC FOR THE HEPATIC STAGES OF *P. FALCIPARUM*
BEARING EPITOPE CAPABLE OF STIMULATING THE T LYMPHOCYTES

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(5') 1 SDLEQERRAKEKLQEQQ
18 SDLEQDRLAKEKLQEQQ
35 SDLEQERLAKEKLQEQQ
52 SDLEQERRAKEKLQEQQ
69 SDLEQERRAKEKLQEQQ
86 SDLEQDRLAKEKLQEQQ
103 SDLEQERRAKEKLQEQQ
120 SDLEQER~~X~~AKEKLQEQQ
137 SDLEQERLAKEKLQEQQ
154 SDLEQERRAKEKLQEQQ
171 SDLEQERRAKEKLQEQQ
188 SDLEQERRAKEKLQEQQ
205 RDLEQ

R

210 RKADTKKNLERKKEHGDLAEDLYGRLEIP
240 AIELPSENERGYYIPHQSSLPQDNRGNSRD
270 SKEISIIEKTNRESITTNVEGRRDIHKGHL
300 EEKKDGSIKPEQKEDKS 316 (3')

FIGURE 1

ANNOTATED SHEET SHOWING CHANGES

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RDEL FNELL NSDV NGEVKENILEE S QVN D IFNSL VJSV QQEQQ
HNVEEK VEESVE ENDEESVE ENVE ENVE ENDGSVASSVEESI
ASSVDESIDSSIEENVAPTV EIVAPTVEEIVAPS VVEKCAPSVE
ESVAPSVEESVAEMLKER

FIGURE 3

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1261 / 421 1291 / 431
AAA GGA AAG AAA TAT GAA AAA ACA AAG GAT AAT TTT AAA CCA AAT GAT AAA AGT TTG
lys gly lys tyr glu lys thr lys asp asn phe lys pro asn asp lys ser leu
1321 / 441 1351 / 451
TAT GAT GAG CAT ATT AAA AAA TAT AAA AAT GAT AAG CAG GTT AAT AAG GAA AAG GAA AAA
tyr asp glu his ile lys lys tyr lys asn asp lys gln val asn lys glu lys glu lys
1381 / 461 1411 / 471
TTC ATA AAA TCA TTG TTT CAT ATA TTT GAC GGA ATT TTA CAG ATC GTG GAT
phe ile lys ser leu phe his ile phe asp glu ile leu gln ile val asp
1441 / 481 1471 / 491
GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA AAG GTT ATA TAT
glu leu ser glu asp ile thr lys tyr phe met lys leu ~~aspartate~~ ~~lys~~ ~~val~~ ~~ile~~ ~~tyr~~

FIGURE 9D

ANNOTATED SHEET SHOWING CHANGES

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LSN. 3' STOP -> 1-phase Translation

DNA sequence 1482 b.p. CAAGAACACAA ... ATGAACTATAA linear

1 / 1 31 / 11 C
 CAA GAA CAA CAA AGC GAT CTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA ~~GAA~~
 gln glu gln ser asp leu glu gln glu arg arg ala lys glu lys leu gln glu gln
 61 / 21 91 / 31
 CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA AAG TTA CAA GAG CAG CAA AGC AGT
 gln ser asp leu glu gln asp arg leu ala lys glu lys leu gln glu gln gln ser asp
 121 / 41 151 / 51
 TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT CTA GAA CAA
 leu glu gln glu arg leu ala lys glu lys leu gln gln ser asp leu glu gln
 181 / 61 211 / 71
 GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT TTA GAA CAA GAG AGA CGT
 glu arg arg ala lys glu lys leu gln gln ser asp leu glu gln gln arg arg
 241 / 81 271 / 91
 GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA
 ala lys glu lys leu gln gln gln ser asp leu glu gln asp arg leu ala lys glu
 301 / 101 331 / 111
 AAG TTA CAA GAG CAG CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA
 lys leu gln gln ser asp leu glu gln glu arg arg ala lys glu lys leu gln

FIGURE 1OA

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1321 / 441 1351 / 451
TAT GAT GAG CAT ATT AAA AAA TAT AAT GAT AAG CAG GTT AAT AAG GAA AAG GAA AAA
tyr asp glu his ile lys lys tyr lys asn asp lys gln val asn lys glu lys glu lys
1381 / 461 1411 / 471
TTC ATA AAA TCA TTG TTT CAT ATA TTT GAC GAC GAA ATT TTA CAG ATC GTG GAT
phe ile lys ser leu phe his ile phe asp gly asp asn glu ile leu gln ile val asp
1441 / 481 1471 / 491
GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA AAG GTT ATA TAT
glu leu ser glu asp ile thr lys tyr phe met lys leu ~~thr~~ ~~lys~~ ~~val~~ ~~ile~~ ~~tyr~~

FIGURE 10D